

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/666,997  
Source: TFW0  
Date Processed by STIC: 09/21/2006

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 09/21/2006

PATENT APPLICATION: US/10/666,997

TIME: 10:59:09

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\09212006\J666997.raw

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3 <110> APPLICANT: Carter, Carol
4      Goff, Arthur
5      Ehrlich, Lorna
6      Cohen, Stanley N.
8 <120> TITLE OF INVENTION: TSG101 AS INHIBITOR OF HIV PRODUCTION
10 <130> FILE REFERENCE: 70017.17USC1
12 <140> CURRENT APPLICATION NUMBER: US 10/666,997
13 <141> CURRENT FILING DATE: 2003-09-18
15 <150> PRIOR APPLICATION NUMBER: PCT/US02/15965
16 <151> PRIOR FILING DATE: 2002-05-21
18 <150> PRIOR APPLICATION NUMBER: US 60/292,761
19 <151> PRIOR FILING DATE: 2001-05-21
21 <160> NUMBER OF SEQ ID NOS: 38
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 391
27 <212> TYPE: PRT
28 <213> ORGANISM: Mouse
30 <400> SEQUENCE: 1
32 Met Ala Val Ser Glu Ser Gln Leu Lys Lys Met Met Ser Lys Tyr Lys
33 1      5      10      15
36 Tyr Arg Asp Leu Thr Val Arg Gln Thr Val Asn Val Ile Ala Met Tyr
37      20      25      30
40 Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr Val Phe Asn Asp Gly Ser
41      35      40      45
44 Ser Arg Glu Leu Val Asn Leu Thr Gly Thr Ile Pro Val Arg Tyr Arg
45      50      55      60
48 Gly Asn Ile Tyr Asn Ile Pro Ile Cys Leu Trp Leu Leu Asp Thr Tyr
49 65      70      75      80
52 Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys Pro Thr Ser Ser Met Thr
53      85      90      95
56 Ile Lys Thr Gly Lys His Val Asp Ala Asn Gly Lys Ile Tyr Leu Pro
57      100     105     110
60 Tyr Leu His Asp Trp Lys His Pro Arg Ser Glu Leu Leu Glu Leu Ile
61      115     120     125
64 Gln Ile Met Ile Val Ile Phe Gly Glu Glu Pro Pro Val Phe Ser Arg
65      130     135     140
68 Pro Thr Val Ser Ala Ser Tyr Pro Pro Tyr Thr Ala Thr Gly Pro Pro
69 145     150     155     160
72 Asn Thr Ser Tyr Met Pro Gly Met Pro Ser Gly Ile Ser Ala Tyr Pro
73      165     170     175
76 Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr Pro Gly Cys Pro Tyr Pro
77      180     185     190

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80 Pro Ala Gly Pro Tyr Pro Ala Thr Thr Ser Ser Gln Tyr Pro Ser Gln
81      195                200                205
84 Pro Pro Val Thr Thr Val Gly Pro Ser Arg Asp Gly Thr Ile Ser Glu
85      210                215                220
88 Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala Val Ser Asp Lys Leu Arg
89 225      230                235                240
92 Trp Arg Met Lys Glu Glu Met Asp Gly Ala Gln Ala Glu Leu Asn Ala
93      245                250                255
96 Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys Gly His Gln Lys Leu Glu
97      260                265                270
100 Glu Met Val Thr Arg Leu Asp Gln Glu Val Ala Glu Val Asp Lys Asn
101      275                280                285
104 Ile Glu Leu Leu Lys Lys Lys Asp Glu Glu Leu Ser Ser Ala Leu Glu
105      290                295                300
108 Lys Met Glu Asn Gln Ser Glu Asn Asn Asp Ile Asp Glu Val Ile Ile
109 305      310                315                320
112 Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu Asn Leu Tyr Ala Glu Glu
113      325                330                335
116 Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu Gly Glu Ala Leu Arg Arg
117      340                345                350
120 Gly Val Ile Asp Leu Asp Val Phe Leu Lys His Val Arg Leu Leu Ser
121      355                360                365
124 Arg Lys Gln Phe Gln Leu Arg Ala Leu Met Gln Lys Ala Arg Lys Thr
125      370                375                380
128 Ala Gly Leu Ser Asp Leu Tyr
129 385      390
132 <210> SEQ ID NO: 2
133 <211> LENGTH: 390
134 <212> TYPE: PRT
135 <213> ORGANISM: Human
137 <400> SEQUENCE: 2
139 Met Ala Val Ser Glu Ser Gln Leu Lys Lys Met Val Ser Lys Tyr Lys
140 1      5      10      15
143 Tyr Arg Asp Leu Thr Val Arg Glu Thr Val Asn Val Ile Thr Leu Tyr
144      20      25      30
147 Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr Val Phe Asn Asp Gly Ser
148      35      40      45
151 Ser Arg Glu Leu Met Asn Leu Thr Gly Thr Ile Pro Val Pro Tyr Arg
152      50      55      60
155 Gly Asn Thr Tyr Asn Ile Pro Ile Cys Leu Trp Leu Leu Asp Thr Tyr
156 65      70      75      80
159 Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys Pro Thr Ser Ser Met Thr
160      85      90      95
163 Ile Lys Thr Gly Lys His Val Asp Ala Asn Gly Lys Ile Tyr Leu Pro
164      100     105     110
167 Tyr Leu His Glu Trp Lys His Pro Gln Ser Asp Leu Leu Gly Leu Ile
168      115     120     125
171 Gln Val Met Ile Val Val Phe Gly Asp Glu Pro Pro Val Phe Ser Arg
172      130     135     140

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175 Pro Ile Ser Ala Ser Tyr Pro Pro Tyr Gln Ala Thr Gly Pro Pro Asn
176 145          150          155          160
179 Thr Ser Tyr Met Pro Gly Met Pro Gly Gly Ile Ser Pro Tyr Pro Ser
180          165          170          175
183 Gly Tyr Pro Pro Asn Pro Ser Gly Tyr Pro Gly Cys Pro Tyr Pro Pro
184          180          185          190
187 Gly Gly Pro Tyr Pro Ala Thr Thr Ser Ser Gln Tyr Pro Ser Gln Pro
188          195          200          205
191 Pro Val Thr Thr Val Gly Pro Ser Arg Asp Gly Thr Ile Ser Glu Asp
192 210          215          220
195 Thr Ile Arg Ala Ser Leu Ile Ser Ala Val Ser Asp Lys Leu Arg Trp
196 225          230          235          240
199 Arg Met Lys Glu Glu Met Asp Arg Ala Gln Ala Glu Leu Asn Ala Leu
200          245          250          255
203 Lys Arg Thr Glu Asp Leu Lys Lys Gly His Gln Lys Leu Glu Glu
204          260          265          270
207 Met Val Thr Arg Leu Asp Gln Glu Val Ala Glu Val Asp Lys Asn Ile
208          275          280          285
211 Glu Leu Leu Lys Lys Lys Asp Glu Glu Leu Ser Ser Ala Leu Glu Lys
212 290          295          300
215 Met Glu Asn Gln Ser Glu Asn Asn Asp Ile Asp Glu Val Ile Ile Pro
216 305          310          315          320
219 Thr Ala Pro Leu Tyr Lys Gln Ile Leu Asn Leu Tyr Ala Glu Glu Asn
220          325          330          335
223 Ala Ile Glu Asp Thr Ile Phe Tyr Leu Gly Glu Ala Leu Arg Arg Gly
224          340          345          350
227 Val Ile Asp Leu Asp Val Phe Leu Lys His Val Arg Leu Leu Ser Arg
228          355          360          365
231 Lys Gln Phe Gln Leu Arg Ala Leu Met Gln Lys Ala Arg Lys Thr Ala
232 370          375          380
235 Gly Leu Ser Asp Leu Tyr
236 385          390
239 <210> SEQ ID NO: 3
240 <211> LENGTH: 5
241 <212> TYPE: PRT
242 <213> ORGANISM: HIV 1
244 <400> SEQUENCE: 3
246 Pro Thr Ala Pro Pro
247 1          5
250 <210> SEQ ID NO: 4
251 <211> LENGTH: 15
252 <212> TYPE: PRT
253 <213> ORGANISM: HIV 1
255 <400> SEQUENCE: 4
257 Ala Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser
258 1          5          10          15
261 <210> SEQ ID NO: 5
262 <211> LENGTH: 35
263 <212> TYPE: DNA

```

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264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Primer
269 <400> SEQUENCE: 5
270 ggctagaagg atccggatgg gtgcgagagc gtcag 35
273 <210> SEQ ID NO: 6
274 <211> LENGTH: 26
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Primer
281 <400> SEQUENCE: 6
282 gaagatctat tagaagttta aagtgc 26
285 <210> SEQ ID NO: 7
286 <211> LENGTH: 26
287 <212> TYPE: DNA
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: Primer
293 <400> SEQUENCE: 7
294 gaagatctca ctacaaaact cttgcc 26
297 <210> SEQ ID NO: 8
298 <211> LENGTH: 30
299 <212> TYPE: DNA
300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Primer
305 <400> SEQUENCE: 8
306 ggaagatctc ccctatagtg cagaacatcc 30
309 <210> SEQ ID NO: 9
310 <211> LENGTH: 23
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Primer
317 <400> SEQUENCE: 9
318 cgggatacctt ccctggcctt ccc 23
321 <210> SEQ ID NO: 10
322 <211> LENGTH: 18
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Primer
329 <400> SEQUENCE: 10
330 gggaagatct ggccttcc 18
333 <210> SEQ ID NO: 11
334 <211> LENGTH: 26
335 <212> TYPE: DNA
336 <213> ORGANISM: Artificial Sequence

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338 <220> FEATURE:
339 <223> OTHER INFORMATION: Primer
341 <400> SEQUENCE: 11
342 gaagatctat tagaagttta aagtgc 26
345 <210> SEQ ID NO: 12
346 <211> LENGTH: 32
347 <212> TYPE: DNA
348 <213> ORGANISM: Artificial Sequence
350 <220> FEATURE:
351 <223> OTHER INFORMATION: Primer
353 <400> SEQUENCE: 12
354 cagagcagac cagagtttct tcagagcaga cc 32
357 <210> SEQ ID NO: 13
358 <211> LENGTH: 30
359 <212> TYPE: DNA
360 <213> ORGANISM: Artificial Sequence
362 <220> FEATURE:
363 <223> OTHER INFORMATION: Primer
365 <400> SEQUENCE: 13
366 cagagcagac cagaggaaga gagcttcagg 30
369 <210> SEQ ID NO: 14
370 <211> LENGTH: 19
371 <212> TYPE: DNA
372 <213> ORGANISM: Artificial Sequence
374 <220> FEATURE:
375 <223> OTHER INFORMATION: Primer
377 <400> SEQUENCE: 14
378 cccctcagag ccaggagcc 19
381 <210> SEQ ID NO: 15
382 <211> LENGTH: 23
383 <212> TYPE: DNA
384 <213> ORGANISM: Artificial Sequence
386 <220> FEATURE:
387 <223> OTHER INFORMATION: Primer
389 <400> SEQUENCE: 15
390 gccgatagac agggaactgt atc 23
393 <210> SEQ ID NO: 16
394 <211> LENGTH: 31
395 <212> TYPE: DNA
396 <213> ORGANISM: Artificial Sequence
398 <220> FEATURE:
399 <223> OTHER INFORMATION: Primer
401 <400> SEQUENCE: 16
402 ccgatagaca aggaaaacga cccctcgta c 31
405 <210> SEQ ID NO: 17
406 <211> LENGTH: 23
407 <212> TYPE: DNA
408 <213> ORGANISM: Artificial Sequence
410 <220> FEATURE:

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**VERIFICATION SUMMARY**

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